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RESULT 9  
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CAGE 941  
PRT: 374 MB.

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T 01-MAR-2001 {TREMBLrel. 16, Created}
T 01-MAR-2001 {TREMBLrel. 16, Last sequence update}
T 01-DEC-2001 {TREMBLrel. 19, Last annotation update}
T 01-DEC-2001 {TREMBLrel. 19, Last sequence update}

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Bacillus licheniformis.  
Bacteria; Firmicutes; Bacillus/Clostridium group;  
Bacillus/Staphylococcus group; Bacillus.

SEQUENCE FROM N.A.  
STRAIN-ATCC12759;  
GENOTYPE-20561724;  
PubMed-11109488;

Can. J. Microbiol. 46:1004-1011(2000).

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R InterPro: IPR000209; Peptidase_S8.  
R Pfam: PF00082; Peptidase_S8; 1.  
R PRINTS: PR00723; SUBTILISIN.  
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[illegible]

RESULT 10  
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CONFIDENTIAL  
REF ID: A66666  
REF ID: A66666

DT	01-MAR-2001	(TREMBLREL. 16, Created)
DT	01-MAR-2001	(TREMBLREL. 16, Last sequence update)
DT	01-DEC-2001	(TREMBLREL. 19, Last annotation update)

OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
DX NCBI\_TaxID=1402;

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ST  
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KL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF282893; AAC00492.1) ; -  
DK HSSP: P00780; 1CSE.

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DR PRINTS: PR00723; SUBTILISIN.  
DR PROSITE: PS00136; SUBTILASE_ASP; 1.  
SQ SEQUENCE 379 AA; 38904 MW; DC65F6A93BDC69CC CRC64;
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Best local Similarity 34.6%; Pred. NO. 3.6e-21;  
Matches 151; Conservative 64; Mismatches 148; Indels 74; Caps

[illegible]



us-09-841-553-5.rspt

Thu Nov 7 10:12:14 2002

[illegible][illegible]











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 AC PROTEIN: 186 (rel. 01. Created)  
 DT 21-JUL-1986 (rel. 01. Last sequence update)  
 DT 16-OCT-2001 (rel. 40. Last annotation update)  
 GN Subtilisin DT (EC 3.4.21.62).  
 OS Bacillus licheniformis.  
 OC Bacillus licheniformis; Bacillus/Clostridium group;  
 OC Bacillus/Firmicutes; Bacillus/Clostridium group; Bacillus.  
 OK MSB\_TaxID=1402;  
 RN SEQUENCE  
 RC STRAIN=IDY;  
 RC MEDLINE=44110064; PubMed=6420308;  
 RT "Primary structure of subtilisin A."  
 RT Hoppe-Jeyar's z. Physiol. Chem. 364:1537-1540(1983).  
 RP X-RAY CRYSTALLOGRAPHY (1.75 ANGSTROMS).  
 RC STRAIN=IDY;  
 RC MEDLINE=50615149; PubMed=9826175;  
 RA Bachemberg S.; Genovese J.; Peters K.; Filtkau S.; Steve S.;  
 RA Wilson K.S.; Betzel C.;  
 RT Carlsberg; Structure of subtilisin Dv, a random mutant of subtilisin  
 RL Eur. J. Biochem. 257:309-318(1998).  
 CC "1" IT CATALYZES THE HYDROLYSIS OF A BROAD SPECTRUM OF PEPTIDES.  
 CC "1" CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS WITH BROAD SPECIFICITY  
 CC IN 10<sup>3</sup> KID BODS, AND A PREFERENCE FOR A LARGE UNCHARGED RESIDUE  
 CC "1" SUBCELLULAR LOCATION: Secreted.  
 CC "1" MISCELLANEOUS: EXPORTION OF SUBTILISIN IS ASSOCIATED WITH ONSET OF  
 CC STAGES AFFECT EXPRESSION LEVELS OF SUBTILISIN. HOWEVER, SUBTILISIN  
 CC "1" IS NOT NECESSARY FOR NORMAL SPORULATION.  
 CC "1" SIMILARITY CLASSIFICATION: SUBTILISIN BELONGS TO PEPTIDASE FAMILY 58; ALSO KNOWN AS THE  
 CC SUBTILASE FAMILY.  
 DR PIR: A05069; SUBSD.  
 DR MEMPRO: 508 001;  
 DR MEMPRO: 508 001;  
 DR InterPro: IP0400209; Peptidase\_S8;  
 DR PRINTS: PR00723; SUBTILISIN; 1;  
 DR PROSITE: PS00116; SUBTILASE\_ABP; 1;  
 DR PROSITE: PS00116; SUBTILASE\_ABP; 1;  
 DR PROSITE: PS00116; SUBTILASE\_ABP; 1;  
 DR Hydrolase: Sporulation: Serine protease, 3D-structure.  
 FT ACT-SITE 32 33 CHARGE RELAY SYSTEM.  
 FT ACT-SITE 220 220 CHARGE RELAY SYSTEM.  
 SQ SEQUENCE 274 AA 27435 MW: 015466622F46533 CMC64;  
 Query Match 15 Gb; Score 535; DB 1; Length 274;  
 Best local Similarity 44.94; Pred. No. 1.2e-33;

Matches 132; Conservative 36; Mismatches 90; Indels 36; Gaps 9;  
 QY 145 WMYHTKGGDSQDGGTIGDITDGLDIPDQKQVQKQVQKQVQKQVQKQVQKQVQKQV 204  
 DB 11 PAKYVQAGQKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 267  
 QY 203 STAGTASQK...VETGAPKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 62  
 DB 68 --AGTVALADMTGVLQVYVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 262  
 QY 263 INLLGSSDSDGQV 340  
 DB 121 IMHGL...GFSCTALKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 177  
 QY 321 AVQNDKNIASFSGPAGDGLKPEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 360  
 DB 178 AVQNDKNIASFSG...ALEVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 222  
 QY 381 THVSGVGLQLQMPSPKPVKLTATVADYAPKEADLQVQVQVQVQVQVQVQV 434  
 DB 223 SHVGAALILSYPTLSQVNNLSSTANUG...SFYQVGLQVQVQVQVQVQV 372  
 RESULT 7  
 ID SUBMITTER STANDARD: PRG: 381 AA.  
 AC PROTEIN: 381 (rel. 01. Created)  
 DT 01-JUN-1994 (rel. 29. Last sequence update)  
 DT 15-DEC-1998 (rel. 37. Last annotation update)  
 GN Subtilisin MAT precursor (EC 3.4.21.62).  
 OS Bacillus subtilis var. natto.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Firmicutes; Bacillus/Clostridium group; Bacillus.  
 OK NCBI\_TaxID=4092;  
 RN [1] FROM N.A.  
 RC STRAIN=IDY;  
 RC MEDLINE=9311005; PubMed=1169031;  
 RA Nucleic Acids Res. 22:1031-1034 (1994).  
 RT Nucleic Acids Res. 22:1031-1034 (1994).  
 CC "1" IT CATALYZES THE HYDROLYSIS OF A BROAD SPECTRUM OF PEPTIDES.  
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 DR PRINTS: PR00723; SUBTILISIN; 1;  
 DR PROSITE: PS00116; SUBTILASE\_ABP; 1;  
 DR PROSITE: PS00116; SUBTILASE\_ABP; 1;  
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 FT ACT-SITE 32 33 CHARGE RELAY SYSTEM.  
 FT ACT-SITE 220 220 CHARGE RELAY SYSTEM.  
 SQ SEQUENCE 381 AA 27435 MW: 015466622F46533 CMC64;  
 Query Match 15 Gb; Score 535; DB 1; Length 274;  
 Best local Similarity 44.94; Pred. No. 1.2e-33;















us-09-841-553-5.rsp

Thu Nov 7 10:12:13 2002

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FT TURN 166 157
FT TURN 176 177
FT STRAND 180 180
FT TURN 188 189
FT TURN 192 195
FT STRAND 204 206
FT TURN 207 211
FT STRAND 213 234
FT TURN 213 234
FT HELIX 237 246
FT TURN 249 249
FT STRAND 254 257
FT HELIX 258 263
FT TURN 264 267
FT TURN 268 267
SQ SEQUENCE 269 AA, 26823 MH; 88AFTLASB25768 CSE64;

Query Match 14.4% Score 631.5; DB 1; Length 269;
Similarity 40.94; Prod No. 2.6e-24;
Matches 121; Conservative 46; Mismatches 92; Indels 37; Gaps 10;

OY 143 KQVATVYVHVLGDSGGTIGTIGDASHPHGQVQKQVDFVMSKSYFDIDGDTN 202
DB 9 ERVQVANNHNGLTGSGVAYATZGI-STBPOL--NRGNATFYQEFSTQDQGNH 65
OY 203 VASTAGTGAASGK-KYGMATKALGIKIVGAGDGGISITIKOVHAYONKDOI 269
DB 65 V---ASTHLLINSIGVLTGSHLAVYLGADQFASISAGLEMDRN---GN 117
OY 261 KYTLGSSGSSDGLSQANNHNGIYVYVAGNSGQPTTFNSPAAKSEVITUC 320
DB 118 HWALLGSSPS--ATLEQANSTKTYVVAASGSGAS--SISYARTANMAY 172
OY 321 AYKSNQKASGSPFADGRLPFTVACQVYINBSGTSMTPTDQVTEASTSMA 380
DB 173 ATQNNHASFSGDAGD-----TVARVNVQSTPGT-----TASLQTSMA 217
OY 383 TPNSGVCALLQAMPSPFTKVTALITPDAVFNKSTADLQNGAGRVYKAK 435
DB 218 IPHWAGMALVKKNPSSNGVIRHLLKFTFISLGTSLC---TSGSLTMDKAT 259

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Search completed: October 31, 2002, 13:30:12  
 Job time: 13 sec

GenCode version 1.1.3

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ON protein - protein search, using sw model

Run on: October 31, 2002, 13:27:48 Search time 17 seconds

Title: US-09-841-553-5  
 Perfect score: 1428  
 Sequence: 1 MGKALIVLVIGLVGVYS.....INSTGQMTQIAVTVIG 659  
 3724-875 Million cell updates/sec

Scoring Table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searches: 283138 seqs, 9608334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2400000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: pr1

2: pr2

3: pr3

4: pr4

Read No. is the number of results predicted by chance to have a score greater than or equal to the score observed. The results are sorted by score, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Length	ID	Description
1	688	201	2 A6587	Intracellular alk
2	595	162	382 1 S08N1	Intracellular alk
3	554	162	379 1 S08N1	subtilisin (EC 3
4	540	158	1388 2 T35159	subtilisin (EC 3
5	537	157	380 2 A45778	high-alkaline ser
6	524	155	34 1 S08SD	subtilisin (EC 3
7	524	155	34 1 S08SD	subtilisin (EC 3
8	524	155	34 1 S08SD	subtilisin (EC 3
9	524	155	34 1 S08SD	subtilisin (EC 3
10	523	153	32 1 J21085	subtilisin (EC 3
11	520	152	381 1 S08N1	subtilisin (EC 3
12	520	152	381 1 S08N1	subtilisin (EC 3
13	520	152	381 1 S08N1	subtilisin (EC 3
14	508	148	361 2 A48323	high-alkaline ser
15	508	148	361 2 A48323	subtilisin-type el
16	505	145	806 2 A41341	subtilisin (EC 3
17	498	143	272 2 A33624	alkaline protease
18	498	143	272 2 A33624	alkaline protease
19	496	145	374 2 T39871	subtilisin (EC 3
20	496	145	374 2 T39871	subtilisin (EC 3
21	488	143	270 2 T39871	serine proteinase
22	485	143	270 2 T39871	serine proteinase
23	485	143	270 2 T39871	serine proteinase
24	485	143	270 2 T39871	serine proteinase
25	485	143	270 2 T39871	serine proteinase
26	485	143	270 2 T39871	serine proteinase
27	485	143	270 2 T39871	serine proteinase
28	485	143	270 2 T39871	serine proteinase
29	485	143	270 2 T39871	serine proteinase

30	443	12.9	440	2	A72784	probable alkaline
31	440	12.8	488	2	A13930	protease [import
32	437	12.8	397	2	A00755	haloalkaliphilic
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37	418	12.2	788	2	T08119	subtilisin-like pr
38	418	12.2	788	2	T08119	subtilisin-like pr
39	411	12.2	921	2	A35690	serine protease
40	411	12.2	921	2	A35690	serine protease
41	409	11.9	325	2	G84006	haloalkaliphilic
42	409	11.9	325	2	G84006	haloalkaliphilic
43	403	11.7	530	2	A44605	subtilisin (EC 3
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45	398	11.6	734	2	T08657	microbial serine p
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ALIGNMENTS

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Page 9

Qy 360 0T8NGZFJ8CITKASQTSMT0PHVSSGVALLOAHPSWPKYKTALETADAVARKEI 419  
DB 292 ---NSTYTGNNVSLCSTSMTPHADVALLKNSRSTNNQSRQSTNCTYLGSPOL 348  
Qy 420 ADIYNGAGBNWYKA 434  
DB 349 ---YGNOLYHAGRA 359

Search completed: October 31, 2002, 13:31:59  
300 time : 21 secs



GenScope version 5.1.3

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DN nucleic - nucleic search, using av model

Run On: November 2, 2002, 05:31:18, Search time 1395.5 seconds  
16947.853 Million cell updates/sec

Title: US-09-841-553-6  
Perfect score: 1777  
Sequence: 1 ATGAGGGGCTGAGACCTCT.....AGCCCTCTCTACTACGGG 1977  
Scoring table: IDENTITY\_NUC Gapop 10.0, Gapext 3.0

Searched: 2004640 seqs, 1455102878 residues

Total number of hits satisfying chosen parameters: 4109780

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.0  
Maximum Match 0.0  
Listing first 45 summaries

Database : Genbank..

- 1: gb-ba\*
- 2: gb-bop\*
- 3: gb-bop\*
- 4: gb-com\*
- 5: gb-com\*
- 6: gb-com\*
- 7: gb-phr\*
- 8: gb-phr\*
- 9: gb-phr\*
- 10: gb-r6\*
- 11: gb-r6\*
- 12: gb-r6\*
- 13: gb-r6\*
- 14: gb-vil\*
- 15: gb-vil\*
- 16: gb-vil\*
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- 45: em-hue\*

Pred. No. is the number of results predicted by chance to have a

scores greater than or equal to the score of the result being printed.  
and is derived by analysis of the data score distribution.

SUMMARIES

Result	Score	Query	Length	DB ID	Description
C 1	1368	65.2	12452	1	AD010265
C 2	1368	68.8	1977	6	AD01155
C 3	1368	68.8	1977	6	AD01155
C 4	68.97	45.3	1236	6	AD01146
C 5	68.97	45.3	1236	6	AD01146
C 6	68.97	45.3	1236	6	AD01146
C 7	197	10.0	4537	1	SS51A07
C 8	197	10.0	4537	1	SS51A07
C 9	197	10.0	4537	1	SS51A07
C 10	141.2	7.1	158053	9	AD01049
C 11	141.2	7.1	158053	9	AD01049
C 12	141.2	7.1	158053	9	AD01049
C 13	134.0	7.1	80900	9	AD01751
C 14	134.0	7.1	80900	9	AD01751
C 15	131.2	6.8	185393	1	SC24
C 16	131.2	6.8	185393	1	SC24
C 17	131.2	6.8	185393	1	SC24
C 18	131.2	6.8	185393	1	SC24
C 19	128.4	6.5	32754	1	SCB4109
C 20	128.4	6.5	32754	1	SCB4109
C 21	128.4	6.5	32754	1	SCB4109
C 22	121.8	6.3	87201	9	AC007623
C 23	121.8	6.3	87201	9	AC007623
C 24	121.8	6.3	87201	9	AC007623
C 25	118	6.0	169143	2	AC11856
C 26	117.9	6.0	181179	9	AL161725
C 27	117.9	6.0	181179	9	AL161725
C 28	116.8	5.9	165317	2	AC058202
C 29	116.8	5.9	165317	2	AC058202
C 30	116.8	5.9	165317	2	AC058202
C 31	111.4	5.6	118853	2	AC03476
C 32	111.4	5.6	118853	2	AC03476
C 33	111.4	5.6	118853	2	AC03476
C 34	105.8	5.6	165034	9	AC058743
C 35	105.8	5.6	165034	9	AC058743
C 36	105.8	5.6	165034	9	AC058743
C 37	105	5.5	150754	9	AC02481
C 38	105	5.5	150754	9	AC02481
C 39	105	5.5	150754	9	AC02481
C 40	107.6	5.4	52550	1	AF00313
C 41	107.6	5.4	52550	1	AF00313
C 42	107.6	5.4	52550	1	AF00313
C 43	107.6	5.4	52550	1	AF00313
C 44	106.4	5.4	184929	9	AC058750
C 45	106.4	5.4	184929	9	AC058750

ALIGNMENTS

Result	Score	Query	Length	DB ID	Description
C 1	1368	65.2	12452	1	AD010265
C 2	1368	68.8	1977	6	AD01155
C 3	1368	68.8	1977	6	AD01155
C 4	68.97	45.3	1236	6	AD01146
C 5	68.97	45.3	1236	6	AD01146
C 6	68.97	45.3	1236	6	AD01146
C 7	197	10.0	4537	1	SS51A07
C 8	197	10.0	4537	1	SS51A07
C 9	197	10.0	4537	1	SS51A07
C 10	141.2	7.1	158053	9	AD01049
C 11	141.2	7.1	158053	9	AD01049
C 12	141.2	7.1	158053	9	AD01049
C 13	134.0	7.1	80900	9	AD01751
C 14	134.0	7.1	80900	9	AD01751
C 15	131.2	6.8	185393	1	SC24
C 16	131.2	6.8	185393	1	SC24
C 17	131.2	6.8	185393	1	SC24
C 18	131.2	6.8	185393	1	SC24
C 19	128.4	6.5	32754	1	SCB4109
C 20	128.4	6.5	32754	1	SCB4109
C 21	128.4	6.5	32754	1	SCB4109
C 22	121.8	6.3	87201	9	AC007623
C 23	121.8	6.3	87201	9	AC007623
C 24	121.8	6.3	87201	9	AC007623
C 25	118	6.0	169143	2	AC11856
C 26	117.9	6.0	181179	9	AL161725
C 27	117.9	6.0	181179	9	AL161725
C 28	116.8	5.9	165317	2	AC058202
C 29	116.8	5.9	165317	2	AC058202
C 30	116.8	5.9	165317	2	AC058202
C 31	111.4	5.6	118853	2	AC03476
C 32	111.4	5.6	118853	2	AC03476
C 33	111.4	5.6	118853	2	AC03476
C 34	105.8	5.6	165034	9	AC058743
C 35	105.8	5.6	165034	9	AC058743
C 36	105.8	5.6	165034	9	AC058743
C 37	105	5.5	150754	9	AC02481
C 38	105	5.5	150754	9	AC02481
C 39	105	5.5	150754	9	AC02481
C 40	107.6	5.4	52550	1	AF00313
C 41	107.6	5.4	52550	1	AF00313
C 42	107.6	5.4	52550	1	AF00313
C 43	107.6	5.4	52550	1	AF00313
C 44	106.4	5.4	184929	9	AC058750
C 45	106.4	5.4	184929	9	AC058750

AD010265 Pyrococcus furiosus DSM 3538, section 140 of 173 of the complete  
AD01155 Pyrococcus furiosus DSM 3538  
AD01146 Pyrococcus furiosus DSM 3538  
SS51A07 Pyrococcus furiosus DSM 3538  
AD01049 Pyrococcus furiosus DSM 3538  
AD01751 Pyrococcus furiosus DSM 3538  
SC24 Pyrococcus furiosus DSM 3538  
SCB4109 Pyrococcus furiosus DSM 3538  
AC007623 Pyrococcus furiosus DSM 3538  
AC11856 Pyrococcus furiosus DSM 3538  
AL161725 Pyrococcus furiosus DSM 3538  
AC058202 Pyrococcus furiosus DSM 3538  
AC03476 Pyrococcus furiosus DSM 3538  
AC058743 Pyrococcus furiosus DSM 3538  
AC02481 Pyrococcus furiosus DSM 3538  
AF00313 Pyrococcus furiosus DSM 3538  
AC058750 Pyrococcus furiosus DSM 3538











Qy 1477 GACTCTGCTACAGCCCTACTAGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1536  
 Db 1081 GACTCTGCTACAGCCCTACTAGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1122  
 Qy 1537 GGAAGCTGCGAGCGCTCAAGCTGCTGACCTACAGAGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1596  
 Db 1341 GGAAGCTGCGAGCGCTCAAGCTGCTGACCTACAGAGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1182  
 Qy 1597 GTTACGACCGAGCGCTGACCGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1200  
 Db 1201 GTTACGACCGAGCGCTGACCGCGCTGCGAGAGCGCTGCTACTACAGCCGACGCC 1182  
 RESULT 5  
 LOCUS AR009704 898 bp DNA Linear PAT 04-DEC-1998  
 DEFINITION Sequence 7 from patent US 5755339.1  
 ACCESSION AR009704  
 VERSION AR009704.1 GI:396509  
 KEYWORDS Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1. (bases 1 to 898)  
 AUTHORS Kato, I., Yamamoto, K., Norishita, M., Ando, K., Tsumasawa, S. and  
 TITLE Hyperthermostable protease gene  
 PATENT US 5755339-A 7 26-MAY-1998  
 FEATURES  
 SOURCE 1. 898  
 BASE COUNT 192 a /organism="unknown"  
 ORIGIN 259 c 380 g 110 t 11 others  
 Query Match 33 94; Score 659.6; db 6; Length 898;  
 Best Local Similarity 85 31; Pred No 2.3e-98  
 Mismatches 780; Conservative 0; Mismatches 118; Indels 6; Gaps 4;  
 Qy 523 GATCTCAAGGAGAGATATGGTGGTACGCTTTGTCATGCTAGGAGCTGATGCTGATG 592  
 Db 1 GATCTCAAGGAGAGATATGGTGGTACGCTTTGTCATGCTAGGAGCTGATGCTGATG 592  
 Qy 593 GATCTCAAGGAGAGATATGGTGGTACGCTTTGTCATGCTAGGAGCTGATGCTGATG 60  
 Db 61 GATCTCAAGGAGAGATATGGTGGTACGCTTTGTCATGCTAGGAGCTGATGCTGATG 60  
 Qy 543 ATGCGAGCTGACGAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 117  
 Db 118 ATGCGAGCTGACGAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 117  
 Qy 703 GCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 702  
 Db 178 GCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 702  
 Qy 763 AGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 237  
 Db 238 AGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 237  
 Qy 833 GCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 822  
 Db 298 GCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 822  
 Qy 883 GTGCG 357  
 Db 338 GTGCG 357  
 Qy 943 AGTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 942  
 Db 418 AGTCTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 942  
 Qy 1003 GCG 1062  
 Db 477 GCG 1062

Db 478 GAGCCAGCG 537  
 Qy 1081 GAGCCAGCG 1122  
 Db 553 GAGCCAGCG 597  
 Qy 1129 TGGAGGACACATGCTGCG 1182  
 Db 558 TGGAGGACACATGCTGCG 657  
 Qy 1188 CAGCG 1242  
 Db 658 CAGCG 716  
 Qy 1243 GCG 1302  
 Db 717 GCG 776  
 Qy 1303 ATGATGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCT 1362  
 Db 777 ATGATGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCTGCGAGCT 836  
 Qy 1363 GCGAGCG 1422  
 Db 837 GCGAGCG 894  
 Qy 1423 AGCG 1426  
 Db 895 AGCG 898  
 RESULT 5  
 LOCUS AR009707  
 DEFINITION AR009707 564 bp DNA Linear PAT 04-DEC-1998  
 ACCESSION AR009707  
 VERSION AR009707.1 GI:3968512  
 KEYWORDS Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1. (bases 1 to 564)  
 AUTHORS Hata, M., Tatemoto, K., Norishita, M., Ando, K., Tsumasawa, S. and  
 TITLE A novel, thermostable protease gene  
 PATENT US 5755339-A 11 26-MAY-1998  
 FEATURES  
 SOURCE 1. 564  
 BASE COUNT 121 a 155 c 161 g 87 t  
 ORIGIN  
 Query Match 21.54; Score 427; db 6; Length 564;  
 Best Local Similarity 18.1; Pred. No 4.3e-99;  
 Mismatches 435; Conservative 75; Indels 3; Gaps 1;  
 Qy 595 GCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 654  
 Db 4 CAGCGAGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 60  
 Qy 655 AGGAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 714  
 Db 61 ATGCGCTGCTGCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 120  
 Qy 715 GCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 774  
 Db 321 GCGAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 180  
 Qy 775 GCGAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 834  
 Db 181 GCGAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 894  
 Qy 835 CTGAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 919















[illegible]



















Library constructed by Dr. Samio Sugano and Dr. Yoichi Kawasumi. DNA Sequencing by Washington University Genome Sequencing Center. Clone distribution information can be found through the I.A.G.E.

Source: GenBank, accession number: U01044.1

Seq primer: TTTT from Narsbar

High quality sequence stop: 527.

Location/Qualifiers

/organism="Homo sapiens"

/clone="541204"

/sex="male"

/dev-stage="adult"

/lib.name="DDB (phase 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

FEATURES

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## RESULT 5

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C MAT05677 standard. DND: 1959 BP.

01-30 2607 /HND; BIRDMIPS //958LYN CIT

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P7 CDS  
 P8 1...1565  
 P9 /Linnal, except- (pos. 1282..1284, aa: Asp)  
 P10 /note= "Xaa= Gly, Val"  
 P11 HQ971832-AL  
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AC AAT08131;  
 DT 10-MAY-1996 (first entry)  
 XX Hypothermostable protease gene.  
 XX Process: Hyperthermostable; thermostability: ss.  
 OS Pyrococcus furiosus.  
 XX Key location/Qualifiers  
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WP0534615-A1  
 XX 21-DEC-1995  
 XX 05-JUN-1995 95NO-JPO1095.  
 XX 26-JUN-1994; 94JP-0173912.  
 XX 13-JUN-1994; 94JP-010235.  
 XX (TAKI) TAKARA SHINGO CO LTD.  
 XX Asada K, Kato T, Mitsu H, Morishita M, Tsumasawa S.  
 PI Tensho K;  
 DK WPI: 1996-045674/05.  
 XX P-FSD0; AAT87009.

PT Pyrococcus furiosus hyperthermostable protease gene - useful for  
 recombinant prodn. of hyperthermostable protease

Example 3: Page 32-53; BspI: Japanese.

The invention relates to the hyperthermostable protease of  
 Pyrococcus furiosus and its prodn. as a recombinant protein  
 and its use. The amino acid sequence of the protease gene  
 (AAT08141). A genomic DNA sequence of the protease gene  
 (AAT08131) and its encoded protein in AAT87009.

50 Sequence 898 BP: 192 A; 299 C; 266 G; 130 T; 11 other.

Query Match 32 94; Score 659.9; Gap 37; Length 898;  
 Best Local Similarity 86.3%; Prod. Max. 60.33%;

Matches 780; Conservative 0; Mismatches 118; Indels 6; Gaps 4;

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Oy 1806 CGCTGAGCTTCGAGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 1865
Db 984 GAGCGAGTACCTGCGCGCGAGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1043
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Search completed: November 7, 2002, 13:09:07  
 Job Line: 8192 reads





APPLICANT: YAMAMOTO, Katsuniko  
 APPLICANT: YAMAMOTO, Katsuniko  
 APPLICANT: ASADA, Kiyoshi  
 APPLICANT: TSUNASHIMA, Susumu  
 TITLE OF INVENTION: HYPERBENEFICIAL PROTEIN GENES  
 NUMBER OF SOURCES: 42  
 ADDRESS: 1-1-1, Higashi-Shinjuku, Shinjuku-ku, Tokyo 162-8601, Japan  
 ADDRESS: 1-1-1, Higashi-Shinjuku, Shinjuku-ku, Tokyo 162-8601, Japan  
 STREET: 4410 Severich Street, N.W., Ste. 300  
 CITY: Washington, D.C.  
 STATE: D.C.  
 COUNTRY: United States of America  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent, Release 1.0, Version 11.30  
 APPLICATION NUMBER: US/09/894,818B  
 FILING DATE: 20-NOV-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP98/03253  
 APPLICATION DATE: 12-DEC-1995  
 APPLICATION NUMBER: JP 327285/1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 11-1996  
 APPLICATION DATE: 12-DEC-1995  
 APPLICATION NUMBER: 11-1996  
 ATTORNEY: Brody, Roger L.  
 REGISTRATION NUMBER: 25,618  
 TELEPHONE: (202) 528-5197  
 TELECOMMUNICATION INFORMATION:  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
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us-09-841-553-6.rn1

Thu Nov 7 10:12:17 2002

TELEPHONE: (202) 928-5197  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
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 STRANDNESS: double  
 MOLECULE TYPE: genomic DNA  
 US-08-894-118a-15

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[illegible]

RESULT 12  
 US-08-94-8198-14 Application US/08948188  
 1 Patent No. 6261832  
 2 GENERAL INFORMATION: 14a  
 3 INVENTOR: KUROKAWA, HIRAFU  
 4 APPLICANT: MORTCHITA, MIO  
 5 APPLICANT: NITTA, MASARU  
 6 APPLICANT: ASADA, MIYUO  
 7 APPLICANT: KATO, TADOSHIGU  
 8  
 9 TITLE OF INVENTION: INTERHEMOSTABLE PROSTATE GLENES  
 10  
 11 ADDRESS: Bromley and Melville  
 12 13000 Melville Road  
 13  
 14 CORRESPONDENCE ADDRESS:  
 15  
 16 STATE: D.C. United States of America  
 17 CITY: Washington  
 18  
 19 ZIP: 20004  
 20  
 21 COMPUTER READABLE  
 22 FORM: YES  
 23 COMPUTER: IBM PC compatible  
 24 SOFTWARE: SPSS  
 25  
 26 CURRENT APPLICATION DATA:  
 27 FILING DATE 08/08/94, 8188  
 28 FILING DATE 20-MAY-1998  
 29  
 30 CLASSIFICATION: 435  
 31 PUBLICATION NO. 08/08/94, 8188  
 32 APPLICATION NUMBER: PCT/JP95/03253  
 33 FILING DATE: 07-NOV-1996

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732  AATTAAAGGAGTCTAGTGGCCCTGGATATACAGTATAGTACGCAATTAGGCTCATTA 701
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491  AATTAAAGGAGTCTAGTGGCCCTGGATATACAGTATAGTACGCAATTAGGCTCATTA 480
734  TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
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```

SEQU 11  
 Sequence 11: Application 05/08150332  
 05-08-750-532-11  
 GENERAL INFORMATION:  
 APPLICANT: MITTU, Norihiko  
 APPLICANT: MITTU, Norihiko  
 APPLICANT: MORENISHI, MIO  
 APPLICANT: ASANO, Naomasa  
 APPLICANT: ASANO, Naomasa  
 APPLICANT: KATO, Ikumiharu  
 TITLE OF INVENTION: HYPERHYPERSTABLE PROTEASE GENE  
 NUMBER OF SEQUENCES: 18  
 CORRESPONDENCE ADDRESS:  
 KATO, IKUMIHARU  
 STREET 415 Seventh Street N.W., Suite 300  
 CITY: Washington  
 COUNTRY: United States of America  
 ZIP: 20004  
 COMMUNICATIONS: TELETYPE  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 SOFTWARE: Microsoft Windows  
 SOFTWARE: Patentlin Release #1.30  
 CURRENT APPLICATION DATA: 05/08150332

```

CLASSIFICATION: 415
PRIOR APPLICATION DATA: PCT/JP99/01095
PRIORITY NUMBER: 76-818-1
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA: JP 1994/130236
PRIORITY NUMBER: 76-818-1
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA: JP 1999/173912
APPLICATION NUMBER: 76-818-1
ATTORNEY/AGENT INFORMATION:
NAME: SHIMIZU NUMBER: 76-818-1
TELEPHONE: 202-331-5508
TELECOMMUNICATION INQUIRY: ALTA-1
REFERENCE/DOCKET NUMBER: 1
TELEFAX: 202-331-5528
INFORMATION FOR SEQ ID NO.: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 554 base pairs
TYPE: nucleic acid
STRATEGY USED: single
SYNTHESIS METHOD: solid phase
MOLECULE TYPE: cDNA
FEATURES: CDS
LOCATION: 1..564
LOCUS: U08-08-730-537-11
Query Match
Best Local Similarity 86.1% Pred No.12e-95
Accession G: M14443e 75, Jule6 3; Cayle
M595 CAGTCAATCATCTGACTTCACGGTGCGAATGACGACAGC 654

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